

GenCore version 4.5
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Om nucleic - nucleic search, using sw model
Run on: March 8, 2002, 14:28:34 ; Search time 1395.32 Seconds
(Without alignments)

11913.912 Million cell updates/sec

Title: US-09-851-670-1
perfect score: 1547
Sequence: 1.999agtccatcatgatcgatg.....tcttacacatagcaggcca 1547
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 11351937 seqs, 5372889281 residues
Total number of hits satisfying chosen parameters: 22703874
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : EST:*

1: em_estfun:*

2: em_estnum:*

3: em_estin:*

4: em_estom:*

5: em_estpl:*

6: em_estba:*

7: em_estroc:*

8: em_estov:*

9: em_htc:*

10: gb_est1:*

11: gb_est2:*

12: gb_htc:*

13: gb_gss:*

14: em_gss_fun:*

15: em_gss_hum:*

16: em_gss_inv:*

17: em_gss_pln:*

18: em_gss_pro:*

19: em_gss_rid:*

20: em_gss_vrt:*

21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Length	DB	ID	Description	RESULT 1	REFERENCE	AUTHORS	DEFINITION	ACCESSION	VERSION	SOURCE	ORGANISM	ALIGNMENTS	
1	612	39.6	670	11	BG874497	BG874497	670 bp mRNA	Homo sapiens	EST	30-MAY-2001	BG8874497.1	GI:14251428			
2	523.4	33.8	876	10	BET79151	BET79151	60146473								
3	507.4	32.8	607	10	AN960221	AN960221									
4	503.8	32.6	1000	10	AL548951	AL548951									
5	502	32.4	1027	10	AL545564	AL545564									
6	458.4	29.6	864	10	AL534146	AL534146									
7	437.8	28.3	948	11	BG686874	BG686874									
8	415	26.8	444	10	AL600183	AL600183									
9	411	26.6	843	11	BG748551	BG748551									
10	408.2	26.4	749	11	BG913158	BG913158									
c	11	403	403	10	AA479072	AA479072									
12	395.6	25.6	1127	11	BG775183	BG775183									

COMMENT
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=t2=RC3-BN0034-120200-012-b03-BN0034>)
primer: puc 18 forward

High quality sequence start: 14
 High quality sequence stop: 669.
 Location/Qualifiers
 1. _670
 /FEATURES source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="BN0034"
 /dev_stage="Adult"
 /note="Organ: breast_normal; Vector: pUC18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 227 a 109 c 164 g 170 t
 ORIGIN

FEATURES	source	BASE COUNT	ORIGIN	Query Match	Score	DB	Length	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps	COMMENT
		156	a	294	96.8%	415	10	98.8%	415	3	98	0	0	This clone (DKFZp313j0132) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES	source	67	c	181	96.4%	313	13	96.4%	313	1	0	0	0	No s1 sequence available.
FEATURES	source	111	g	181	96.4%	313	13	96.4%	313	1	0	0	0	1. .44
FEATURES	source	110	t	181	96.4%	313	13	96.4%	313	1	0	0	0	2. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	3. .44
BASE COUNT				Db	61	96.4%	313	13	96.4%	313	1	0	0	4. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	5. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	6. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	7. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	8. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	9. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	10. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	11. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	12. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	13. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	14. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	15. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	16. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	17. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	18. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	19. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	20. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	21. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	22. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	23. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	24. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	25. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	26. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	27. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	28. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	29. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	30. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	31. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	32. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	33. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	34. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	35. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	36. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	37. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	38. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	39. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	40. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	41. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	42. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	43. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	44. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	45. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	46. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	47. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	48. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	49. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	50. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	51. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	52. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	53. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	54. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	55. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	56. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	57. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	58. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	59. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	60. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	61. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	62. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	63. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	64. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	65. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	66. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	67. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	68. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	69. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	70. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	71. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	72. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	73. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	74. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	75. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	76. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	77. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	78. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	79. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	80. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	81. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	82. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	83. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	84. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	85. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	86. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	87. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	88. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	89. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	90. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	91. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	92. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	93. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	94. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	95. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	96. .44
BASE COUNT				QY	99	96.4%	313	13	96.4%	313	1	0	0	97. .44
BASE COUNT				Db	181	96.4%	313	13	96.4%	313	1	0	0	98. .44
BASE COUNT				QY	99	96.4%	313							

COMMENT

Contact: Wilson RK

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This clone is available royalty-free through LInL; contact the

IMAGE Consortium (<http://image.llnl.gov>) for further information.

Seq primer: -41ml3 fwd. Fwd from Amersham

High quality sequence stop: 370.

FEATURES SOURCE

1 .403

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Search completed: March 8, 2002, 21:05:19
Job time: 23805 sec